

Amendment and Response

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For: INDUCIBLE LIGAND FOR $\alpha 1\beta 1$ INTEGRIN AND USES

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Amendments to the Specification

Please replace the paragraph beginning at page 16, line 21, with the following amended paragraph.

As stated above, active analogs include polypeptides having structural similarity (i.e., sequence identity). Structural similarity is generally determined by aligning the residues of the two amino acid sequences to optimize the number of identical amino acids along the lengths of their sequences; gaps in either or both sequences are permitted in making the alignment in order to optimize the number of identical amino acids, although the amino acids in each sequence must nonetheless remain in their proper order. Preferably, two amino acid sequences are compared using the NCBI BLASTB, version 2.2.6, of the BLAST 2 search algorithm. Preferably, the default values for all BLAST 2 search parameters are used with slight variations for Protein: Search for Short Nearly Exact Matches available on the word wide web at http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi?CMD=Web&LAYOUT=TwoWindows&AUTO_FORMAT=Semiauto&ALIGNMENTS=50&ALIGNMENT_VIEW=Pairwise&CLIENT=web&DATABASE=nr&DESCRIPTIONS=100&ENTREZ_QUERY=%28none%29&EXPECT=20000&FORMAT_OBJECT=Alignment&FORMAT_TYPE=HTML&GAPCOSTS=9+1&I_THRESHOLD=0.005&MATRIX_NAME=PAM30&NCBI_GI=on&PAGE=Proteins&PROGRAM=blastp&SERVICE=plain&SET_DEFAULTS.x=24&SET_DEFAULTS.y=10&SHOW_OVERVIEW=on&WORD_SIZE=2&END_OF_HTTPGET=Yes&SHOW_LINKOUT=yes&GET_SEQUENCE=yes including matrix = PAM30; open gap penalty = 10, extension gap penalty = 1, expect = 20000, wordsize = 3, and filter on= low complexity. In the comparison of two amino acid sequences using the BLAST search algorithm, structural similarity is referred to as "identity."